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2	840.6	25.2	1069	14	B0278843	AGENCODR
3	705	21.1	705	14	BM830016	K-EST010
4	675	20.2	687	14	BM791383	K-EST0077
5	666	20.0	689	14	BM791435	K-EST0077
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C	7	596.8	17.9	936	14	B0954456	AGENCOCURT
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C	29	503.8	15.1	611	10	BB618558	BB618558 BB618558
C	30	498.2	14.9	555	10	AM9666212	AM9666212 EST378285
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C	33	492.8	14.8	507	12	BE799819	BE799819 RC2-FT004
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C	35	488.4	14.6	528	12	BF744823	BF744823 QV2-BT063
C	36	485.6	14.6	493	14	BM855444	BM855444 C-EST0138
C	37	485	14.5	892	12	BF535659	BF535659 602054056
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C	39	481	14.4	493	9	A1889507	A1889507 wN05d10 x
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RESULT 1
AK017241

LOCUS	AK017241	1773 bp	mRNA	linear	HFC 19-JAN-2003
DEFINITION	Mus musculus adult male pituitary gland cDNA, RIKEN full-length enriched library, clone:5330417C22:homolog to KIAA1324 PROTEIN (FRAGMENT), full insert sequence.				

ACCESSION	AK017241
VERSION	AK017241.1
GI	GI:12856379

SOURCE Mus musculus (strain:C57BL/6J) adult male pituitary gland cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:5330417C2.

ORGANISM

REFERENCE
1
AUTHORS
TITLE
JOURNAL
Carninci, P. and Hayashiaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus

REFERENCE

TITLE
JOURNAL
MEDLINE
PUBMED

Itch, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

20499374
11042159

REFERENCE	AUTHORS
3	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, H., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujie, S., Inoue, K., Togawa, Y., Iwawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kiru, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system---384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shitagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 11217851
 5 (bases 1 to 1773)
 Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,

TITLE
JOURNAL

Direct Submission
Submitted (10-Jul-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, url: <http://genome.gsc.riken.go.jp/>, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT
Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'] GAGCAGACGAGAAGATCCAAAGACTCTCTTTTGTTCCTTTTN 3'], cDNA was prepared by using triphase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'

GAAGAGAGAGAGTTCGAGTAAATTAATTAATTAATGCCCCCCCCCCC 3'. cDNA was cleaved with BamHI and XhoI. Vector: a modified pInescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

location/Qualifiers

1..1773

Source

1.1773

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OY 1600 GTGGCTGTGAATTCTTNGAGCAACACACTCCTGTGGAGACGTTGGAAGGTTCCAAAGGCAAA 1659
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QY 1720 AGGACCACTTTTCATGAGGCAAGCAGGAAGTACACCAATGACGTTGCCAAGATCTTACTCC 1779
 DB 181 AGGACCACTTTTCATGAGGCAAGCAGGAAGTATCTAAAGATGCTGCCAAGATCTACTCA 240

1780 ATCATGTCACCAATGTTATGAATGGCGTGGCTCTACTGCGCTCCCTGTGCCTAGAA 1839
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[illegible][illegible]

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Db	421	GCACAGGGCTGTGTGCCCCGTGGTCCAGGAGACCAAGAAATACCAAGATGCATCTCTCTCTG	480
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Db	481	TACACGACGTGACCTTCTCCGAAACACCCCGAGAGGTTTTCAACTGACACTTCTCA	540
Qy	2080	GCTTTTGGCAACACCGTCTACTCTTGTGTGAGAGGCCAAGCTTCACCTTCCAAAGGGTTGAA	2139

Db 541 GCTCTGGCAGGCACCGCTCTCTCTCTGCGAGGGGTGCCGAGCTTCACTTCGAAAGGGGCTGAAG 600

QY 2140 TACTTTCATCACTTTACCTCGAGTCTCTGGAAGCAGGGTAGGAAAATGTCCTGTGTC 2199

Db 601 TATTTTCATCATTTTCAACCTCGAGTCTCTGTGCAAAACCAAGGGGAAAAAATGGCTGTGTGC 660

QY 2200 ACGACAAATGCTACGTACCTCGGATTCCTCGAGGTGAGTCAAGGCTTCTCCAAATCTATC 2259

Db 661 ACAGACAATGCTACTGACCTCCGATCCCTGATGAGGCGGCTTCTCTAATCCGTC 720

QY 2260 ACAGCTACGCTGTGCGAGGAGATCATCCGCCAGAGGAGTACAAAGCGCGG 2319

Db 721 ACAGCTACGCTGTGCGAGGAGTGTATCATCTCTCTGATGATGGCTACAAAGCGCGG 780

QY 2320 GTTTCCTACAGGCTGTGAGGCTGTGATGATGATTTGGGGGAGACACAGATGACT 2379

Db 781 GTGCTCTACAGCTGTGAGGCTGTGATGATGATTTGGGGGAGACACAGATGACT 839

QY 2380 CTGATGGAATACACTGCCAGCTGCAACTTTTCACCTGAGATCTTGGGAATACGGAC 2439

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Db 951 ACCATCCGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1010

QY 2560 ACAGCTACGCTGTGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2619

Db 1011 ATGAGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1070

QY 2620 GCTTCCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2679

Db 1071 GCTTCCCGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1130

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QY 3157 GCGATTTGGGAGGCGAGC-ATGCTGCAACACCATGCTGTAATGCTTTCATTTGTTGGCT 3215

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RESULT 2
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DEFINITION AGENCOURT_7049684 NIH_MGC_107 Homo sapiens cDNA clone IMAGE:5805500
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VERSION BQ278843.1 GI:20489051
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC <http://mhc.nci.nih.gov/>.
1 (bases 1 to 1069)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM2044 row: m column: 21
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Site:2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcORI/XhoI sites using the
following 5' adaptor: GGCACAG(G). Library constructed by
Ling Hong in the Laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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VERSION BM830016.1 GI:19186425
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 705)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology

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52 Eooun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsungemail.kribb.re.kr
Plate: 17 row: E column: 12
High quality sequence stop: 705.
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Site:2: NotI; The poly (A) + RNA was dephosphorylated with
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with tabacco acid pyrophosphatase (TAP). The deapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library. After analyzing and
sequencing about 2,000 ~ 3,000 colonies in original cDNA
library, the abundant cDNAs were selected and amplified by
PCR reaction using vector region primer including T7
promotor as 5' primer and Ndt114 as 3' primer. The PCR
products were used as template for synthesis of
bioinylated single stranded RNA by in vitro transcription
reaction. The synthesized RNA probes were hybridized with
antisense single stranded cDNAs prepared from original
library and incubated with avidin gel. After removing
DNA-RNA hybrids by centrifuge, the substracted cDNA
libraries were constructed by transformation of the
remaining DNA into competent cells E. coli Top10F with
electroporation method."
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KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	1 (bases 1 to 689) Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE	21C Frontier Korean Est Project 2001
JOURNAL	Unpublished (2002)
COMMENT	Contact: Kim YS Genome Research Center 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409 Email: yongsung@mail.kribb.re.kr Plate: 20 Row: A Column: 12 High quality sequence stop: 689.
FEATURES	Location/Qualifiers 1..689 /organism="Homo sapiens" /db_xref="taxon.9606" /clone="S21SN0520-20-A12" /clone_11b="S21SN0320" /sex="F" /tissue_type="Stomach" /cell_type="Floating aggregates" /cell_line="SNU-520" /lab_host="Top10F" Note="Organ: Stomach; Vector: pTZ189PL; Site_1: EcoRI; Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tabacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoRI I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformaton of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
BASE COUNT	151 a 211 c 154 g 173 t
ORIGIN	
Query Match	20.0%; Score 666; DB 14; Length 689;
Best Local Similarity	99.7%; Pred. No. 2.1e-143;
Matches 688; Conservative	0; Mismatches 0; Indels 2; Gaps 2;
1802	ATGGCGTGGCCCTCTACTAGCCGCTCCCTGTGCGCCTTAGAAGCCCTGTGATGTGGCTCTCCT 1861
1862	GCACCTCTTGTCTCTGCTGGTACTATATTGACCGAGATTCCAGAACCTGCCACTCTCTGCC 1921
61	GCACCTCTTGTCTCTGCTGGTACTATATTGACCGAGATTCCAGAACCTGCCACTCTCTGCC 120
1922	CCCCTAACCAATTCCTGAAAGCCCAACAGCCCTTAAGTGCTGCCAGCCCTGTGCGCCTGTG 1981
121	CCCCTAACCAATTCCTGAAAGCCCAACAGCCCTTAAGTGCTGCCAGCCCTGTGCGCCTGTG 180
1982	GTCCAGGAGCAACAACAAGATCCACTCTCTGTGCTACTAATGATGTCACCTTCTCAC 2041
181	GTCCAGGAGCAACAACAAGATCCACTCTCTGTGCTACTAATGATGTCACCTTCTCAC 240
2042	GGAACATCCACACGAGACTTTCACATCAACTCTCCGCTTTGGCAACACGCGACATC 2101
241	GGAACATCCACACGAGACTTTCACATCAACTCTCCGCTTTGGCAACACGCGACATC 300

Query	Match	Score	DB	Length	Match
QY	2102	TTGCTGGAAGGGCCAAAGCTTCACCTTCCAAAGGGTGAATTA	CCCTTACCTTCACCTTACCCTCA	2161	
Db	301	TTGCTGGAAGGGCCAAAGCTTCACCTTCCAAAGGGTGAATTA	CCCTTACCTTCACCTTACCCTCA	360	
QY	2162	GTCCTCTGGAAGAACAGGGTGAAGAAATGTCTGTGTGCAC	CGACAAATGTCACTGACCTCC	2221	
Db	361	GTCCTCTGGAAGAACAGGGTGAAGAAATGTCTGTGTGCAC	CGACAAATGTCACTGACCTCC	420	
QY	2222	GGATTCTGAGGGGTGAGTCAGGGTTCTCCAATCTATACAG	CCCTAGCTTCGCCAGCGAG	2281	
Db	421	GGATTCTGAGGGGTGAGTCAGGGTTCTCCAATCTATACAG	CCCTAGCTTCGCCAGCGAG	480	
QY	2282	TCATCATCCCCCCAGAGTGTGACAGGCTACAA-GGGCGGG	GTTCCTCTCACACCTTCCAGC	2340	
Db	481	TCATCATCCCCCCAGAGTGTGACAGGCTACAA-GGGCGGG	GTTCCTCTCACACCTTCCAGC	540	
QY	2341	CTTGCTGATCGACTTATTTGGGGGTGACAACAGATATGAC	TCCTGTGATGACCTCCCA	2400	
Db	541	CTTGCTGATCGACTTATTTGGGGGTGACAACAGATATGAC	TCCTGTGATGACCTCCCA	600	
QY	2401	GCTGACCTTTTCCACCTTGAGATCCTTGGGAATACCGGAG	CGAGATCTTCTTTATAGTCC	2460	
Db	601	GCTGACCTTTTCCACCTTGAGATCCTTGGGAATACCGGAG	CGAGATCTTCTTTATAGTCC	659	
QY	2461	AATGATGTGACCAAGTCTGCAGTTCTGGG	2490		
Db	660	AATGATGTGACCAAGTCTGCAGTTCTGGG	689		
RESULT 6					
LOCUS	AV751975	685 bp	mRNA	linear	EST 19-OCT-2000
DEFINITION	AV751975 NPJ Homo sapiens cDNA clone NPDBGR09 5', mRNA sequence.				
ACCESSION	AV751975				
VERSION	AV751975.1	GI:10909823			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 685)				
AUTHORS	Song,H., Peng,Y., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Ye,M., Zhang,Q., Han,Z., Chen,Z., Hu,R. and Chen,J.				
TITLE	Homo sapiens NPJ library cDNA clones				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Qinghua Zhang Shanghai Institute of Endocrinology, Rui-Jin Hospital 197 Rui-Jin II Road, Shanghai 200025, P. R. China Tel: 86-21-64370045(ex.663332) Fax: 86-21-64743206 Email: mbsheims.stn.sh.cn This clone is available at Shanghai Hematology Institute in Shanghai. Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong.				
FEATURES	Location/Qualifiers				
SOURCE	1..685				
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	/clone="NPDBGR09"				
	/clone_lib="NPJ"				
	/tissue_type="Pituitary"				
	/dev_stage="Adult"				
	/lab_host="SOLR"				
	/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"				
BASE COUNT	145 a 194 c 173 g 169 t 4 others				
ORIGIN					
Query Match	18.8%;	Score 625.2;	DB 10;	Length 685;	

Best Local Similarity 96.8%; Pred. No. 5.8e-134;
Matches 658; Conservative 0; Mismatches 17; Indels 5; Gaps 2;

QY 2043 CAACACCTCCACACCGAGACTTTCACATCACTTCTCCGCTTGGCAAAACCGCTCATCT 2102
Db 1 CAACACCTCCACACCGAGACTTTCACATCACTTCTCCGCTTGGCAAAACCGCTCATCT 59
QY 2103 TGTGTGAGAGGCGCAAGCTTCACTTCCAAAGGCTTGAATTAATCTTCATCACTTACCTCCAG 2162
Db 60 TGTGTGAGAGGCGCAAGCTTCACTTCCAAAGGCTTGAATTAATCTTCATCACTTACCTCCAG 119
QY 2163 TCTCTGTGGAAGCAAGGCTAGAAATGTCTGTGTGACCGACAATGTCACTGACTCCG 2222
Db 120 TCTCTGTGGAAGCAAGGCTAGAAATGTCTGTGTGACCGACAATGTCACTGACTCCG 179
QY 2223 GATTTCCTGAGGCTGATGACAGGCTTCTCCAAATCTATACAGCCTTACCTGCGACGT 2282
Db 180 GATTTCCTGAGGCTGATGACAGGCTTCTCCAAATCTATACAGCCTTACCTGCGACGT 239
QY 2283 CATCATCCCCCGACAGGCTGACAGGCTCAAGGCGGGGTTTCTCACAGCCTGACAGCT 2342
Db 240 CATCATCCCCCGACAGGCTGACAGGCTCAAGGCGGGGTTTCTCACAGCCTGACAGCT 299
QY 2343 TGTGTGATGACTTATTTGGGGTGACACAGATATGACTCTGATGGAATCACTCCGACG 2402
Db 300 TGTGTGATGACTTATTTGGGGTGACACAGATATGACTCTGATGGAATCACTCCGACG 359
QY 2403 TGACCTTTTCCACTGAGTCTTGGGAATACCGGACGTATCTCTTTTATATAGTCCAA 2462
Db 360 TGAACCTTTTCCACTGAGTCTTGGGAATACCGGACGTATCTCTTTTATATAGTCCAA 419
QY 2463 TGATGTGACCCAGTCTGACAGTCTTGGGAGATCAACACCATCGGCTGACGAGTCC 2522
Db 420 TGATGTGACCCAGTCTGACAGTCTTGGGAGATCAACACCATCGGCTGACGAGTCC 479
QY 2523 ACAGAAAACGTCTCCCTGGAAGTTTGTCTGTGCCAGAACTGTCTCAGATGGAGCTGTGA 2582
Db 480 ACAG----CTGTCTCCCTGGAAGTTTGTCTGTGCCAGAACTGTCTCAGATGGAGCTGTGA 535
QY 2583 TGGCTGCAACCTTCCACTTCTCTGTGGGAGAGAGCGGGCTGTCTGCTGCTCACTGAGC 2642
Db 536 TGGCTGCAACCTTCCACTTCTCTGTGGGAGAGAGCGGGCTGTCTGCTGCTCACTGAGC 595
QY 2643 TGACTACCATGCTATCTGCTGACAGCTGTGTGGCTGGGATCCAGAAAGACTTACGTGTG 2702
Db 596 TGACTACCATGCTATCTGCTGACAGCTGTGTGGCTGGGATCCAGAAAGACTTACGTGTG 655
QY 2703 GCGGAAACCAAGCTATGCT 2722
Db 656 GCGGAAACCAAGCTATGCTGTGT 675

RESULT 7

B0954456

LOCUS

DEFINITION

B0954456 936 bp mRNA linear EST 21-AUG-2002

AGENCOURT_8879471 NCI_CGAP_Co24 Mus musculus cDNA clone

IMAGE:6476084 5', mRNA sequence.

B0954456.1 GI:22369934

KEYWORDS

EST.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: gcrabs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14015 row: n column: 21
High quality sequence stop: 674.

FEATURES
source
1. 936
Location/Qualifiers

/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6476084"
/clone_id="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1; NotI;
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP library."
BASE COUNT 207 a 260 c 239 g 226 t 4 others
ORIGIN

Query Match 17.9%; Score 596.8; DB 14; Length 936;
Best Local Similarity 85.9%; Pred. No. 2.1e-127;

Matches 672; Conservative 0; Mismatches 109; Indels 1; Gaps 1;

QY 2331 GCCTGACAGCTTGTGATGACATTTTGGGGTGACACAGATATGACTCTGATGGAAT 2390
Db 1 GCGCTGACAGCTTGTGATGACATTTTGGGGTGACACAGATATGACTCTGATGGAAT 60
QY 2391 CACCTCCCGACGAGCACTTTCACACTGAGTCTTGGGAATACCGGACGTATCTTCT 2450
Db 61 CCGCTCCCGACGAGCACTTTCACACTGAGTCTTGGGAATACCGGACGTATCTTCT 120
QY 2451 TTATAGTCCAAATGATGTGACCCAGTCTGACAGTCTTGGGAGATCAACACCATCCGCT 2510
Db 121 TTATAGTCCAAATGATGTGACCCAGTCTGACAGTCTTGGGAGATCAACACCATCCGCT 180
QY 2511 CAGGTGCACTCCACAGAAACGTCTCCCTGGAAGTTTGTCTGCTGCCAGAGACTGCTCAGA 2570
Db 181 CAGGTGCACTCCACAGAAACGTCTCCCTGGAAGTTTGTCTGCTGCCAGAGACTGCTCAGA 240
QY 2571 TGGGACCTGTGATNGGCTGCAACTTCCACTTCTGTGGGAGAGCGGGCTGTGGCCCT 2630
Db 241 TGGGACCTGTGATNGGCTGCAACTTCCACTTCTGTGGGAGAGAGTGTGGCCCTGTGGCACT 300
QY 2631 CTGCTCAGTGTGCTGACTACCATGCTATGTGTGACAGAGCTGTGTGGCTGGGATCCAGAAC 2690
Db 301 CTGCTCAGTGTGCTGACTACCATGCTATGTGTGACAGAGCTGTGTGGCTGGGATCCAGAAC 360
QY 2691 TACTTACGTGTGGGAGAACCCAGCTATGCTCTGTGGCAATTTCTTCCCTGACAGAG 2750
Db 361 TACTTACGTGTGGGAGAACCCAGCTATGCTCTGTGGCAATTTCTTCCCTGACAGAG 420
QY 2751 ACTCACCATCTGCAAAACCATAGATTCTGTGGCTGAAATGGGACATCTGTGAGGACCTG 2810
Db 421 ACTTACCATCTGCAAAACCATAGATTCTGTGGCTGAAATGGGACATCTGTGAGGACCTG 480
QY 2811 TACTGCAATCTGTCTACCCGCTTGTGACCTGCTACTTTTGGAAAAAAGTAACAAAACCTAGA 2870
Db 481 TACTGCAATCTGTCTACCCGCTTGTGACCTGCTACTTTTGGAAAAAAGTAACAAAACCTAGA 540
QY 2871 GTTCAAGTACCTGCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2930
Db 541 GTTCAAGTACCTGCAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
QY 2931 TGACAGCTGCGCCATCATGAGAGGAGAGATGAGAGAGACCTCATCTTTACACGAA 2990
Db 601 AGACAGCTGTGCGCCATCATGAGAGAGAGAGAGAGAGATGATGATGATGATGATGATGATGATGAT 660
QY 2991 GAA-TTACTCTTTTGGGAAAGATCAATCAATTTTACTTCCAGAGAGACTCTGTATGATTTGA 3049
Db 661 GAAATCCCTTTTGGGAAAGATCAATCAATTTTACTTCCAGAGAGACTCTGTATGATTTGA 720

QY	3050	CTCACTGGCGGTGAGACATCTCTGTGTGACAGAGGCCCAACATGTGAGTGAAGGACCTGCC	3109
Db	721	CTCGGTGCGCGGTGAGAGACGTCTTACAGAGAGGCCCAACATGTGAGTGAAGGCTGCC	780
QY	3110	TG 3111	
Db	781	CG 782	
RESULT 8			
LOCUS	AM994023	653 bp	mRNA
DEFINITION	RC3-BN0036-090200-011-b10 BN0036 Homo sapiens CDNA, mRNA sequence.		
ACCESSION	AM994023		
VERSION	AM994023.1	GI:8254218	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 653) Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bata, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.		
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)		
MEDLINE	20202663		
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-27049922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?pl=4t2-RC3-BN0036-090200-011-b10&t3=2000-02-09&t4=1) Seq primer: puc 18 forward High quality sequence start: 43 High quality sequence stop: 652. Location/Qualifiers 1. .653 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="BN0036" /dev_stage="Adult" /note="Organ: breast; normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."		
FEATURES			
source			
BASE COUNT	160 a 171 c 183 g 139 t		
ORIGIN			
Query Match	17.8%: Score 593.8; DB 10; Length 653;		
Best Local Similarity	99.3%; Pred No. 1,1e-126;		
Matches 607; Conservative	0; Mismatches 2; Indels 2; Gaps 1;		
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QY	2236	GAGTCAGGGTTCCTCAATCTATACACAGCTACGTGTGCGCAGGACATCATATCCCCCA	2295
Db	593	GAGTCAGGGTTCCTCAATCTATACACAGCTACGTGTGCGCAGGACATCATATCCCCCA	534

QY	2236	GAGGTGACAGGCTACAAAGCCGGGGTTTCCTCACAAGCTCGACGCTTGCGATCGACTT	2355
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QY	2356	ATTGGGGGACAAACAGATATGACTCTGGATGGAAATCAACCTCCAGCGTAACCTTTTCAC	2415
Db	473	ATTGGGGGACAAACAGATATGACTCTGGATGGAAATCAACCTCCAGCGTAACCTTTTCAC	414
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QY	2476	TTCGCTCACTTCTGGGAGATCAACCAACCATTCGCGCGACGTGACGTCACAGAAAACTGC	2535
Db	353	TTCGCTCACTTCTGGGAGATCAACCAACCATTCGCGCGACGTGACGTCACAGAAAACTGC	294
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Db	293	CCTGGAAATTTTGCTGCTCCACGAAACGTCACAGATGGGACCTGTGATGCTGCACCTTC	234
QY	2596	CACCTTCCTGTGGGAGAGCGCGGCTGCTCCCGCTGCTCAGTGGGCTGACTACATCT	2655
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QY	2656	ATCGTCACACAGCTGTGTGGCTGGGATCCAGAAAGACTTACTGCTGTGGCGAACCAG	2715
Db	173	ATCGTCACACAGCTGTGTGGCTGGGATCCAGAAAGACTTACTGCTGTGGCGAACCAG	116
QY	2716	CTATGCTGTGTGGTGCATTTCTCTGCTTGACGACAGAGATCCACATCTGCAAAACCTATAT	2775
Db	115	CTATGCTGTGTGGTGCATTTCTCTGCTTGACGACAGAGATCCACATCTGCAAAACCTATAT	56
QY	2776	TTTCTGGCTGAA	2786
Db	55	TTTCTGGCTGAA	45
RESULT	9		
LOCUS	BE969851	609 bp	linear
DEFINITION	6016794251 NIH_MGC_78 Homo sapiens cDNA clone IMAGE:3949710 5',		
ACCESSION	BE969851	RNA sequence.	
VERSION	BE969851.1	GI:10582784	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 609)		
JOURNAL	NIH-MGC http://imgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strussberg, Ph.D.		
	Email: cs9abs@remail.nih.gov		
	Tissue Procurement: CLONETECH Laboratories, Inc.		
	cDNA Library Preparation: CLONETECH Laboratories, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: ILCM815 row: a column: 07		
	High quality sequence stop: 607.		
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	/clone="IMAGE:3949710"		
	/clone_1lb="NIH_MGC_78"		
	/lab_host="DH10B (TI phage-resistant)"		
	/note="Organ: pancreas; Vector: pBNR-LIB (Clontech);"		

